

SEQUENCE LISTING

<110> Paul Moore et al.

<120> Methods and Compositions for Treating and Preventing Infection
Using Human Interferon Regulatory Factor 3

<130> PF196P1

<140> Unassigned

<141> 2001-10-12

<150> 60/239,963

<151> 2000-10-13

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1426

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (47)..(1327)

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Pro Lys Pro Arg Xaa Leu Pro Trp Leu Val Ser Gln Leu Asp Leu Gly
5 10 15

caa ctg gag ggc gtg gcc tgg gtg aac aag agc cgc acg cgc ttc cgc 151
Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr Arg Phe Arg
20 25 30 35

atc cct tgg aag cac gcc cta cgg cag gat gca cag cag gag gat ttc 199
Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln Glu Asp Phe
40 45 50

gga atc ttc cag gcc tgg gcc gag gcc act ggt gca tat gtt ccc ggg 247
Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr Val Pro Gly
55 60 65

agg gat aag cca gac ctg cca acc tgg aag agg aat ttc cgc tct gcc 295
Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe Arg Ser Ala
70 75 80

ctc aac cgc aaa gaa ggg ttg cgt tta gca gag gac cgg agc aag gac Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg Ser Lys Asp 85 90 95	343
cct cac gac cca cat aaa atc tac gag ttt gtg aac tca gga gtt ggg Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser Gly Val Gly 100 105 110 115	391
gac ttt tcc cag cca gac acc tct cgg gac acc aat ggt gga ggc agt Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly Gly Lys Ser 120 125 130	439
act tct gat acc cag gaa gac att ctg gat gag tta ctg ggt aac atg Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu Gly Asn Met 135 140 145	487
gtg ttg gcc cca ctc cca gat cgg gga ccc cca agc ctg gct gta gcc Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu Ala Val Ala 150 155 160	535
cct gag ccc tgc cct cag ccc ctg cgg agc ccc agc ttg gac aat ccc Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu Asp Asn Pro 165 170 175	583
act ccc ttc cca aac ctg ggg ccc tct gag aac cca ctg aag cgg ctg Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu Lys Arg Leu 180 185 190 195	631
ttg gtg cgg ggg gaa gag tgg gag ttc gag gtg aca gcc ttc tac cgg Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala Phe Tyr Arg 200 205 210	679
ggc cgc caa gtc ttc cag cag acc atc tcc tgc cgg gag ggc ctg cgg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu Gly Leu Arg 215 220 225	727
ctg gtg ggg tcc gaa gtg gga gac agg acg ctg cct gga tgg cca gtc Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly Trp Pro Val 230 235 240	775
aca ctg cca gac cct ggc atg tcc ctg aca gac agg gga gtg atg agc Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly Val Met Ser 245 250 255	823
tac gtg agg cat gtg ctg agc tgc ctg ggt ggg gga ctg gct ctc tgg Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu Ala Leu Trp 260 265 270 275	871
cgg gcc ggg cag tgg ctc tgg gcc cag cgg ctg ggg cac tgc cac aca Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His Cys His Thr 280 285 290	919
tac tgg gca gtg agc gag gag ctg ctc ccc aac agc ggg cat ggg cct Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly His Gly Pro 295 300 305	967
gat ggc gag gtc ccc aag gac aag gaa gga ggc gtg ttt gac ctg ggg Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe Asp Leu Gly 310 315 320	1015

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ccc ttc att gta gat ctg att acc ttc acg gaa gga agc gga cgc tca 1063
Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser Gly Arg Ser
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cca cgc tat gcc ctc tgg ttc tgt gtg ggg gag tca tgg ccc cag gac 1111
Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp Pro Gln Asp
340 345 350 355

cag ccg tgg acc aag agg ctc gtg atg gtc aag gtt gtg ccc acg tgc 1159
Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val Pro Thr Cys
360 365 370

ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc tcc tcc ctg 1207
Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala Ser Ser Leu
375 380 385

gag aat act gtg gac ctg cac att tcc aac agc cac cca ctc tcc ctc 1255
Glu Asn Thr Val Asp Leu His Ile Ser Asn Ser His Pro Leu Ser Leu
390 395 400

acc tcc gac cag tac aag gcc tac ctg cag gac ttg gtg gag ggc atg 1303
Thr Ser Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val Glu Gly Met
405 410 415

gat ttc cag ggc cct ggg gag agc tgagccctcg ctccctcattg tgtgcctcca 1357
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35 40 45

Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
50 55 60

Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
65 70 75 80

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Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
 85 90 95
 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
 100 105 110
 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
 115 120 125
 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
 130 135 140
 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
 145 150 155 160
 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
 165 170 175
 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
 180 185 190
 Lys Arg Leu Leu Val Pro Gly Glu Trp Glu Phe Glu Val Thr Ala
 195 200 205
 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
 210 215 220
 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
 225 230 235 240
 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
 245 250 255
 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
 260 265 270
 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
 275 280 285
 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
 290 295 300
 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
 305 310 315 320
 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
 325 330 335
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
 340 345 350
 Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
 355 360 365
 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
 370 375 380
 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Ser Asn Ser His Pro
 385 390 395 400

Leu	Ser	Leu	Thr	Ser	Asp	Gln	Tyr	Lys	Ala	Tyr	Leu	Gln	Asp	Leu	Val
				405					410					415	
Glu	Gly	Met	Asp	Phe	Gln	Gly	Pro	Gly	Glu	Ser					
			420					425							

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